in the fynbos. The present study sets out to investigate the diversity of mites associated with three *Protea* species located in the Hottentots-Holland Mountains. The key questions addressed include a) how do ecological and host morphology influence mite communities within *Protea* spp. infructescences? b) Can bio-geographical patterns and/or patterns of host specificity be detected between mite populations? and, c) Is there genetic evidence for co-evolution between various *Protea* spp. and mites (focusing on the economically important mite genus *Tarsonemus*)? Significant differences in infructescence volume and degree of openness (causing differences in humidity) between *P. repens*, *P. nitida* and *P. neriifolia* have been detected. Within-species differences were also detected between different populations in terms of mite communities present within infructescences. Different host species harbour different mite communities with a significant difference between *P. neriifolia* and *P. nitida*. This study will form the basis for future studies on mite-insect-*Protea*-fungal interactions.

doi:10.1016/j.sajb.2009.02.112

Keetia (Rubiaceae subfam. Ixoroideae, tribe Vanguerieae) in southern Africa - an update on the classification and selected recently-studied structural features

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The genus *Keetia* E.Phillips has a single representative in southern Africa, namely *K. gueinzii* (Sond.) Bridson. It is a robust climber, scrambling shrub or small tree, associated with forest and thicket. *Keetia*, together with *Psydrax*, *Afrocanthium* and *Canthium s. str.*, were for many years included in *Canthium s. l.* The main differences between the southern African representatives of these genera are highlighted. The anatomy of calycine colleters in *K. gueinzii* is described. Structural features of the stylar head, which is involved in secondary pollen presentation, are elucidated and compared with existing descriptions. Controversy surrounding the terminology for describing the prominent protruding apertures of fresh pollen grains, is mentioned. In *K. gueinzii*, endophytic bacterial symbiosis was recently discovered, this being a first report in the leaves of a *Keetia*.

doi:10.1016/j.sajb.2009.02.113

The status of *Aloe dichotoma* subsp. *dichotoma* (quiver tree) populations in Goegap Nature Reserve

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The quiver tree *Aloe dichotoma* subsp. *dichotoma* is the aesthetic icon that dominates the landscape in the Northern Cape. Concern has been expressed that *A. dichotoma* populations are not recruiting well and this decline has been linked to climate change. Other claims on the death of *A. dichotoma* have been reported to be caused by the fungal pathogens such as aloe rust. The Goegap Nature Reserve is a protected area of the Northern Cape Province that falls on the summer-winter rainfall transition. The aim of the study was to evaluate the status of three quiver tree populations in the Goegap Nature Reserve and to try to determine the growth rate of the quiver trees through repeat photography. Demographic and health characters of approximately 100 individuals per population were recorded for each of the three populations on the reserve. The size structures of the different populations were determined in terms of height, basal circumference and crown diameter. The effects of leaf damage, pests and fungal infections will be discussed. An attempt was made to relate specific recruitment opportunities to climatic conditions of a particular year.

doi:10.1016/j.sajb.2009.02.114

Genetic analysis of an *Arabidopsis thaliana* ecotype showing resistance to a bacterial wilt isolate from *Eucalyptus*

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Ralstonia solanacearum is a soilborne, vascular pathogen infecting several hosts including many economical important plants. Previous work has revealed a novel pathosystem between a *Eucalyptus* isolate of *R. solanacearum* (BCCF 402) and the *Arabidopsis thalaiana* ecotypes Bensheim (Be-0) and Killean (Kil-0). Isolate BCCF 402 caused severe wilt symptoms and killed Be-0 two weeks after infection, while Kil-0 was identified as the resistant ecotype remaining healthy two weeks after infection. The main objective of this study was to characterize the genetic basis of resistance in Kil-0 to the isolate BCCF 402. Genetic crosses between Be-0 and Kil-0 and subsequent pathogen challenges revealed a 1:3 segregation of resistance: susceptibility in the F2 progeny, suggesting that resistance was caused by a single recessive gene. A previous study indicated that resistance to the tomato isolate GMI1000 of *R. solanacearum*, in a cross between *A. thaliana* ecotypes Col-5 and Nd-1, also segregated as a simply inherited recessive trait, and *RRS1-R* was identified as the major determinant of resistance against this isolate. We have identified allelic differences between *RRS1* loci in the two ecotypes Kil-0 and Be-0. The Kil-0 allele segregates with the resistant phenotype in

the F2 progeny, indicating that a *RRS1-R* allele may play a role in conferring resistance against isolate BCCF 402.

doi:10.1016/j.sajb.2009.02.115

The role and regulation of the tricarboxylic acid cycle in *Solanum lycopersicum* roots

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Carbon, fixed from the biosphere, need to be converted to biochemically diverse compounds to sustain energy and life. As a central link in this process, the tricarboxylic acid (TCA) cycle operates to convert carbon from glycolysis to organic acids, driving energy and reductant provision as a primary product. However, these organic acids (e.g. malate, citrate, pyruvate, succinate, fumarate, 2-ketoglutarate, isocitrate and aconitate) are also connected to pathways that extend beyond this central process. In this study, carbon partitioning was investigated in tomato (*Solanum lycopersicum* cv. Moneymaker) roots that were down-regulated at individual steps of the tricarboxylic acid (TCA) cycle. Constitutive antisense inhibition of mitochondrial malate dehydrogenase (EC 1.1.1.37), fumarase (EC 4.2.1.2), succinyl coA ligase (EC 6.2.1.5), mitochondrial citrate synthase (EC 4.1.3.7) and aconitase (EC 4.2.1.3) were characterised by exhibiting ca. 50% residual total NAD^+-dependent MDH activity, between 25-50% residual fumarase activity, between 16-66% residual succinyl coA ligase activity, between 6-60% residual aconitase activity, and between 25-56% total citrate synthase activity, respectively. In addition, due to isoform specificity and subcellular localisation considerations, the down-regulation of protein activity in the mitochondrial enriched fraction was illustrated for fumarase and aconitase, whilst the reduced expression of malate dehydrogenase and citrate synthase was confirmed for the mitochondrial isoform via quantitative reverse-transcription polymerase chain reaction. These transgenic sets were further evaluated for specific root attributes. This demonstrated that these manipulations resulted in differences in root growth with all the transgenics being characterized by a dramatic reduction in root dry matter deposition and respiratory activity. Modulation of malate metabolism additionally resulted in opposite changes with respect to root area in mitochondrial malate dehydrogenase and fumarase lines. A range of physiological, molecular and biochemical experiments were carried out in order to determine whether changes in root attributes were due to altered metabolism within the root itself, alterations in the nature of the transformants root exudation, consequences of alteration in the efficiency of photoassimilate delivery to the root or a combination of these factors. Grafting experiments in which the transformants were reciprocally grafted to wild type controls suggested that root length and area could be partially controlled by the aerial part of the plant but that biomass was not. Decreased biomass assimilation could much more likely be related to reduced root respiration measurements and cellulose content. In addition, despite the transgenic roots displaying alteration in the expression of phytohormone associated genes, evaluation of the levels of the hormones themselves in mitochondrial malate dehydrogeanse and fumarase lines revealed that, with the exception of gibberellins, they were largely unaltered. When taken together these combined experiments suggest that root biomass and growth are retarded by root specific alterations in energy metabolism and gibberellin content.

doi:10.1016/j.sajb.2009.02.116

Radiation-induced genome alterations in *Vigna unguiculata*

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Seeds from an inbred cowpea cultivar (*Vigna unguiculata*) were irradiated with a dose of 180Gy. The irradiated seeds were sow in the field and through consecutive seasons selected for increased drought tolerance (Spreeth, ARC). The result was a number of lines (8) that showed improved drought tolerance. Three techniques, RAPD, RDA and SSRs were use to evaluate the DNA variation among the selected mutants and non-irradiated control plants in order to gain an understanding of the response and the DNA repair mechanism of the cowpea genome to gamma radiation. A range of putative radiation-induced genome changes have been isolated and characterized. Detected variations included point mutations, rearrangements of long arrays of repetitive sequences, length polymorphisms, deletions and possible mobilization of transposable elements. Furthermore, a large number of M1 irradiated individuals were PCR screened to investigate the frequency of irradiation-linked mutations without selection pressure in a number of identified polymorphic regions. Detailed analysis of all characterized regions indicated that the rate at which various regions of the genome are mutated in irradiation experiments can differ significantly. Therefore, the genome does not appear to be randomly rearranged in response to the irradiation stress. Some regions, like the chloroplast regions appear to be very susceptible to irradiation damage and we might speculate that these regions act as a mutation buffer under various forms of stress.

doi:10.1016/j.sajb.2009.02.117